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* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *
FILE 'HOME' ENTERED AT 16:21:35 ON 10 MAR 2004
=> file biosis,caba,caplus,embase,japio,lifesci,medline,scisearch,uspatfull
=> e groot anne de/au
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E3            3 --> GROOT ANNE DE/AU
E4            1     GROOT ANNE KLAAS DE/AU
E5            1     GROOT ANNE S DE/AU
E6            1     GROOT ARIEN/AU
E7            2     GROOT ARJAN/AU
E8            1     GROOT ARJAN J/AU
E9            1     GROOT ART/AU
E10          11     GROOT ARTHUR/AU
E11           1     GROOT ARTHUR H J P/AU
E12          15     GROOT ASTRID T/AU
=> s e3-e5 and mycobact?
L1            3 ("GROOT ANNE DE"/AU OR "GROOT ANNE KLAAS DE"/AU OR "GROOT ANNE
                S DE"/AU) AND MYCOBACT?
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2            3 DUP REM L1 (0 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y
 L2   ANSWER 1 OF 3  USPATFULL on STN
AN     2002:336878  USPATFULL
TI     Human T cell response to MHC-binding motif clusters
IN       ***Groot, Anne De***  , Providence, RI, UNITED STATES
PI     US 2002192233      A1   20021219
AI     US 2001-44703      A1   20011109 (10)
RLI    Continuation of Ser. No. US 2001-813333, filed on 20 Mar 2001, PENDING
PRAI   US 2000-190834P     20000320 (60)
DT     Utility
FS     APPLICATION
LREP   MINTZ LEVIN, One Financial Center, Boston, MA, 02111
CLMN   Number of Claims: 12
ECL    Exemplary Claim: 1
DRWN   7 Drawing Page(s)
LN.CNT 1431
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The invention provides   ***Mycobacterium***   tuberculosis (Mtb)
       vaccine candidate peptides. The invention also provides a method for
       identifying Mtb vaccine candidate peptides as well as vaccines
       comprising these Mtb candidate peptides.

L2   ANSWER 2 OF 3  USPATFULL on STN
AN     2002:322061  USPATFULL
TI     HIV vaccine candidate peptides
IN       ***Groot, Anne De***  , Providence, RI, UNITED STATES
PI     US 2002182222      A1   20021205
AI     US 2001-55524      A1   20011026 (10)
RLI    Division of Ser. No. US 1999-351036, filed on 9 Jul 1999, PENDING
PRAI   US 1998-92346P      19980710 (60)
       US 1999-115145P     19990108 (60)
       US 1999-130677P     19990423 (60)
DT     Utility
FS     APPLICATION
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LREP   MINTZ, LEVIN, COHN, FERRIS,, GLOVSKY and POPEO, P.C., One Financial
       Center, Boston, MA, 02111
CLMN   Number of Claims: 12
ECL    Exemplary Claim: 1
DRWN   11 Drawing Page(s)
LN.CNT 2025
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The invention provides HIV vaccine candidates that have "evolved" due to
       gene shuffling in vitro for inclusion of "cross-clade" characteristics.
       The invention also provides a method for identifying HIV vaccine
       candidates that could be presented in the context of more than one HLA,
       due to the creation of promiscuous epitopes by gene shuffling.

L2   ANSWER 3 OF 3  USPATFULL on STN
AN     2002:221025  USPATFULL
TI     Human T cell response to MHC-binding motif clusters
IN       ***Groot, Anne De***  , Providence, RI, UNITED STATES
PI     US 2002119160      A1   20020829
AI     US 2001-813333     A1   20010320 (9)
PRAI   US 2000-190834P     20000320 (60)
DT     Utility
FS     APPLICATION
LREP   MINTZ, LEVIN, COHN, FERRIS, GLOVSKY and POPEO, P.C, One Financial
       Center, Boston, MA, 02111
CLMN   Number of Claims: 12
ECL    Exemplary Claim: 1
DRWN   4 Drawing Page(s)
LN.CNT 1408
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The invention provides   ***Mycobacterium***   tuberculosis (Mtb)
       vaccine candidate peptides. The invention also provides a method for
       identifying Mtb vaccine candidate peptides as well as vaccines
       comprising these Mtb candidate peptides.


=> e de groot anne/au
E1            1     DE GROOT ANE JAN/AU
E2            1     DE GROOT ANGELIQUE/AU
E3            7 --> DE GROOT ANNE/AU
E4            2     DE GROOT ANNE KLAAS/AU
E5           45     DE GROOT ANNE S/AU
E6           12     DE GROOT ANNEMIEKE A/AU
E7            3     DE GROOT ANNETTE M B/AU
E8            1     DE GROOT ANTHONIUS DANIEL/AU
E9            1     DE GROOT ANTHONY J/AU
E10           3     DE GROOT ANTON/AU
E11          29     DE GROOT ANTON C/AU
E12           2     DE GROOT ANTON J/AU

=> s e3-e5 and mycobact?
L3           10 ("DE GROOT ANNE"/AU OR "DE GROOT ANNE KLAAS"/AU OR "DE GROOT
                ANNE S"/AU) AND MYCOBACT?

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4             8 DUP REM L3 (2 DUPLICATES REMOVED)
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=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 8 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:449835 BIOSIS
DN PREV200100449835
TI From genome to vaccine: In silico predictions, ex vivo verification.
AU ***De Groot, Anne S.*** [Reprint author]; Bosma, Andrew; Chinai, Natasha; Frost, Julie; Jesdale, Bill M.; Gonzalez, Michael A.; Martin, William; Saint-Aubin, Caitlin
CS TB/HIV Research Laboratory, Brown University, Providence, RI, 02912, USA anne_degroot@brown.edu
SO Vaccine, (14 August, 2001) Vol. 19, No. 31, pp. 4385-4395. print. CODEN: VACCDE. ISSN: 0264-410X.
DT Article
LA English
ED Entered STN: 19 Sep 2001
Last Updated on STN: 22 Feb 2002
AB Bioinformatics tools enable researchers to move rapidly from genome sequence to vaccine design. EpiMer and EpiMatrix are computer-driven pattern-matching algorithms that identify T cell epitopes. Conservatrix, BlastiMer, and Patent-Blast permit the analysis of protein sequences for highly conserved regions, for homology with other known proteins, and for homology with previously patented epitopes, respectively. Two applications of these tools to epitope-driven vaccine design are described in this review. Using Conservatrix and EpiMatrix, we analyzed more than 10000 HIV-1 sequences and identified peptides that were potentially immunostimulatory and highly conserved across HIV-1 clades. MHC binding assays and CTL assays have been carried out: 50 (69%) of the 72 candidate epitopes bound in assays with cell lines expressing the corresponding MHC molecule; 15 of the 24 B7 peptides (63%) stimulated gamma-interferon release in ELISpot assays. These results lend support to the bioinformatics approach to selecting novel, conserved, HIV-1 CTL epitopes. EpiMatrix was also applied to the entire 'proteome' derived from two ***Mycobacterium*** tuberculosis (Mtb) genomes. Using EpiMatrix, BlastiMer, and Patent-Blast, we narrowed the list of putative Mtb epitopes to be tested in vitro from 1 600 000 to 3000, a 99.8% reduction. The pace of vaccine design will accelerate when these and other bioinformatics tools are systematically applied to whole genomes and used in combination with in vitro methods for screening and confirming epitopes.

L4 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1996:399095 BIOSIS
DN PREV199699121451
TI A novel algorithm for the efficient identification of T-cell epitopes: Prediction and testing of candidate tuberculosis vaccine peptides in genetically diverse populations.
AU ***De Groot, Anne S.*** [Reprint author]; Roberts, Caroline G. P. [Reprint author]; Edelson, Brian T. [Reprint author]; Meister, Gabriel E. [Reprint author]; Jesdale, Bill M. [Reprint author]; Houghten, Richard A.; Carter, E. Jane; Montoya, Jaime; Romulo, Rodriguo C.; Berzofsky, Jay A.; Ramirez, Bernadette D. L. L.
CS TB/HIV Res. Lab., Int. Health Inst., Brown Univ. Sch. Med., Providence, RI 02912, USA
SO Brown, F. [Editor]; Norrby, E. [Editor]; Burton, D. [Editor]; Mekalanos, J. [Editor]. Vaccines (Cold Spring Harbor), (1996) pp. 127-134. Vaccines (Cold Spring Harbor); Molecular approaches to the control of infectious

diseases.
Publisher: Cold Spring Harbor Laboratory Press, 10 Skyline Drive, Plainview, New York 11803, USA. Series: Vaccines (Cold Spring Harbor). Meeting Info.: Thirteenth Meeting. Cold Spring Harbor, New York, USA. September 13-17, 1995.
ISSN: 0899-4056. ISBN: 0-87969-479-3.

DT Book
Conference; (Meeting)
Book; (Book Chapter)
Conference; (Meeting Paper)

LA English

ED Entered STN: 3 Sep 1996
Last Updated on STN: 3 Sep 1996

L4 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1996:453255 CAPLUS

DN 125:165218

TI A novel algorithm for the efficient identification of T-cell epitopes: Prediction and testing of candidate tuberculosis vaccine peptides in genetically diverse populations

AU ***De Groot, Anne S.*** ; Roberts, Caroline G. P.; Edelson, Brian T.; Meister, Gabriel E.; Jesdale, Bill M.; Houghten, Richard A.; Carter, E. Jane; Montoya, Jaime; Romulo, Rodriguo C.; et al.

CS School Medicine, Brown University, Providence, RI, 02912, USA

SO Vaccines 96: Molecular Approaches to the Control of Infectious Diseases, [Meeting on the Molecular Approaches to the Control of Infectious Diseases], 13th, Cold Spring Harbor, N. Y., Sept. 13-17, 1995 (1996), Meeting Date 1995, 127-134. Editor(s): Brown, Fred. Publisher: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y.
CODEN: 63CVAY

DT Conference

LA English

AB The relation between clustering of MHC-binding motifs and immune responses provide support for the use of motif matching computer-driven algorithms, such as EpiMer, to predict promiscuous or "universal" epitopes. The EpiMer algorithm was used to successful predict known T-cell epitopes in ***Mycobacterium*** tuberculosis proteins. The algorithm also predicted
epitopes that have not been previously investigated.

L4 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1995:466350 BIOSIS

DN PREV199598480650

TI Two novel MHC-binding motif-based T-cell epitope prediction algorithms: Prediction of epitopes for six ***Mycobacterium*** tuberculosis protein antigens.

AU Meister, Gabriel E. [Reprint author]; Roberts, Caroline G. P. [Reprint author]; Edelson, Brian T. [Reprint author]; Berzofsky, Jay A.; ***De*** *** Groot, Anne S.*** [Reprint author]

CS TB/HIV Res. Lab., Brown Univ., Providence, RI 02912, USA

SO Chanock, R. M. [Editor]; Brown, F. [Editor]; Ginsberg, H. S. [Editor]; Norrby, E. [Editor]. Vaccines (Cold Spring Harbor), (1995) pp. 219-226. Vaccines (Cold Spring Harbor); Molecular approaches to the control of infectious diseases.
Publisher: Cold Spring Harbor Laboratory Press, 10 Skyline Drive, Plainview, New York 11803, USA. Series: Vaccines (Cold Spring Harbor). Meeting Info.: Twelfth Annual Meeting on Modern Approaches to New

Vaccines. Cold Spring Harbor, New York, USA. October 1994.
ISSN: 0899-4056. ISBN: 0-87969-467-X.
DT Book
Conference; (Meeting)
Book; (Book Chapter)
Conference; (Meeting Paper)
LA English
ED Entered STN: 1 Nov 1995
Last Updated on STN: 1 Nov 1995

L4 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
AN 1995:345683 BIOSIS
DN PREV199598359983
TI Two novel T cell epitope prediction algorithms based on MHC-binding motifs: Comparison of predicted and published epitopes from ***Mycobacterium*** tuberculosis and HIV protein sequences.
AU Meister, Gabriel E. [Reprint author]; Roberts, Caroline G. P. [Reprint author]; Berzofsky, Jay A.; ***De Groot, Anne S.***
CS TB/HIV Res. Lab., Brown Univ., Providence, RI 02912, USA
SO Vaccine, (1995) Vol. 13, No. 6, pp. 581-591.
CODEN: VACCDE. ISSN: 0264-410X.
DT Article
LA English
ED Entered STN: 10 Aug 1995
Last Updated on STN: 10 Aug 1995
AB We have designed two computer-based algorithms for T cell epitope prediction, OptiMer and EpiMer, which incorporate current knowledge of MHC-binding motifs. OptiMer locates amphipathic segments of protein antigens with a high density of MHC-binding motifs. EpiMer identifies peptides with a high density of MHC-binding motifs alone. These algorithms exploit the striking tendency for MHC-binding motifs to cluster within short segments of each protein. Putative epitopes predicted by these algorithms contain motifs corresponding to many different MHC alleles, and may contain both class I and class II motifs, features thought to be ideal for the peptide components of synthetic subunit vaccines. In this study, we describe the use of OptiMer and EpiMer for the prediction of putative T cell epitopes from ***Mycobacterium*** tuberculosis and human immunodeficiency virus protein antigens, and demonstrate that these two algorithms may provide sensitive and efficient means for the prediction of promiscuous T cell epitopes that may be critical to the development of vaccines against these and other pathogens.

L4 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:839727 CAPLUS
DN 123:311759
TI Two novel MHC-binding motif-based T-cell epitope prediction algorithms: Prediction of epitopes for six ***Mycobacterium*** tuberculosis protein antigens
AU Meister, Gabriel E.; Roberts, Caroline G. P.; Edelson, Brian T.; Berzofsky, Jay A.; ***De Groot, Anne S.***
CS TB/HIV Research Laboratory, Brown University, Providence, RI, 02912, USA
SO Vaccines 95: Molecular Approaches to the Control of Infectious Diseases, [Annual Meeting on Molecular Approaches to the Control of Infectious Diseases], 12th, Cold Spring Harbor, N. Y., Oct., 1994 (1995), Meeting Date 1994, 219-26. Editor(s): Chanock, Robert M. Publisher: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y.

CODEN: 61TGAQ
DT Conference; General Review
LA English
AB A review with 7 refs. on the T-cell epitope predictive power of two algorithms, OptiMer and EpiMer. ***Mycobacterium*** tuberculosis antigens were used as sample antigens.

L4 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1994:149553 BIOSIS
DN PREV199497162553
TI A longitudinal study of in vitro immune response to ***Mycobacterium*** tuberculosis in HIV-seropositive subjects.
AU Fisher, Kimberly A. [Reprint author]; Phair, John P.; ***De Groot, Anne*** *** S.***
CS Brown Univ., Providence, RI, USA
SO Journal of Cellular Biochemistry Supplement, (1994) Vol. 0, No. 18B, pp. 131.
Meeting Info.: Keystone Symposium on Prevention and Treatment of AIDS. Hilton Head Island, South Carolina, USA. January 23-30, 1994.
ISSN: 0733-1959.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 30 Mar 1994
Last Updated on STN: 30 Mar 1994

L4 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 2
AN 1993:469423 BIOSIS
DN PREV199345092548
TI T-cell responses to ***Mycobacterium*** tuberculosis antigens in the HIV-infected host.
AU ***De Groot, Anne S.*** [Reprint author]; McGowan, Katherine; Scheib, Rochelle G.; Schmid, Chris H.; Lieberman, Judy; Wyler, David J.
CS Div. Geographic Med. Infect. Dis., New England Med. Center. Hosp., Boston, MA 02111, USA
SO Ginsberg, H. S. [Editor]; Brown, F. [Editor]; Chanok, R. M. [Editor]; Lerner, R. A. [Editor]. Vaccines (Cold Spring Harbor), (1993) pp. 251-257. Vaccines (Cold Spring Harbor); Modern approaches to new vaccines including prevention of AIDS.
Publisher: Cold Spring Harbor Laboratory Press, 10 Skyline Drive, Plainview, New York 11803, USA. Series: Vaccines (Cold Spring Harbor).
Meeting Info.: Tenth Annual Meeting. Cold Spring Harbor, New York, USA. September 1992.
ISSN: 0899-4056. ISBN: 0-87969-383-5.
DT Article
Conference; (Meeting)
LA English
ED Entered STN: 11 Oct 1993
Last Updated on STN: 11 Oct 1993

=> e degroot anne/au
E1 1 DEGROOT ALICE A/AU
E2 1 DEGROOT ANDREAS R/AU
E3 4 --> DEGROOT ANNE/AU

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E4            5      DEGROOT ANNE S/AU
E5            2      DEGROOT ANTHONY J/AU
E6            1      DEGROOT ANTON C/AU
E7            1      DEGROOT ARCHIBALD/AU
E8           60      DEGROOT B/AU
E9            7      DEGROOT B D/AU
E10           2      DEGROOT B F/AU
E11          13      DEGROOT B J/AU
E12          16      DEGROOT B L/AU

=> s e3-e4 and mycobact?
L5            3 ("DEGROOT ANNE"/AU OR "DEGROOT ANNE S"/AU) AND MYCOBACT?

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6            3 DUP REM L5 (0 DUPLICATES REMOVED)

=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L6   ANSWER 1 OF 3  USPATFULL on STN
AN     2003:257264  USPATFULL
TI     Immunogenic, cross-clade, HIV peptides
IN       ***DeGroot, Anne***  , Providence, RI, UNITED STATES
PI     US 2003180314      A1   20030925
AI     US 2002-200708     A1   20020722 (10)
RLI    Continuation-in-part of Ser. No. US 1999-351036, filed on 9 Jul 1999,
       ABANDONED
PRAI   US 1998-92346P      19980710 (60)
       US 1999-115145P     19990108 (60)
       US 1999-130677P     19990423 (60)
DT     Utility
FS     APPLICATION
LREP   LUANN CSERR, LAW OFFICE OF LUANN CSERR, SUITE 100, 166 WHEELER AVENUE,
       CRANSTON, RI, 02905-2710
CLMN   Number of Claims: 20
ECL    Exemplary Claim: 1
DRWN   8 Drawing Page(s)
LN.CNT 5326
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The invention provides Cross-clade candidates that have "evolved" due to
       gene shuffling in vitro for inclusion of "cross-clade" characteristics.
       The invention also provides a method for identifying Cross-clade
       candidates that could be presented in the context of more than one HLA,
       due to the creation of promiscuous epitopes by gene shuffling.

L6   ANSWER 2 OF 3  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2002:634271  BIOSIS
DN   PREV200200634271
TI   Computational methods for mapping T cell epitopes in the
       ***Mycobacterium***  tuberculosis proteome: A streamlined approach to
     vaccine design.
AU   Sbai, Hakima [Reprint author]; McMurry, Julie [Reprint author]; Martin,
     Bill; Rayner, James; Sherman, David R.;  ***DeGroot, Anne S.***
     [Reprint author]
CS   TB/HIV Research Lab, Brown University, Providence, RI, USA
SO   Tuberculosis (Edinburgh), (2002) Vol. 82, No. 2-3, pp. 123-124. print.
```

Meeting Info.: 36th Annual Research Conference of the US-Japan Cooperative Medical Science Program Tuberculosis and Leprosy Panel. Louisiana, USA. July 15-17, 2001.
ISSN: 1472-9792.

DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 12 Dec 2002
Last Updated on STN: 12 Dec 2002

L6 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:713381 CAPLUS
DN 135:271885
TI Predicting T-cell epitopes of ***Mycobacterium*** tuberculosis for vaccines using EpiMer algorithm
IN ***Degroot, Anne S.***
PA Brown University Research Foundation, USA
SO PCT Int. Appl., 42 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001070774	A2	20010927	WO 2001-US8906	20010320
	WO 2001070774	A3	20020228		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 2002119160	A1	20020829	US 2001-813333	20010320
	EP 1268532	A2	20030102	EP 2001-918859	20010320
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	US 2002192233	A1	20021219	US 2001-44703	20011109
PRAI	US 2000-190834P	P	20000320		
	US 2001-813333	A1	20010320		
	WO 2001-US8906	W	20010320		

AB The invention provides ***Mycobacterium*** tuberculosis (Mtb) vaccine candidate peptides. The invention also provides a method for identifying Mtb vaccine candidate peptides as well as vaccines comprising these Mtb candidate peptides. These peptides are recognized by HLA class II antigens and induce anti- ***Mycobacterium*** antibody responses. The peptides were selected using EpiMer, a computer-based algorithm for predicting T-cell epitopes by searching for clusters of MHC binding motifs.